GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: February 11, 2005, 16:40:34 ; Search time 359 Seconds
(without alignments)
5738.357 Million cell updates/sec

Title: US-09-824-134-1_COPY_388_735
Perfect score: 348
Sequence: 1 TTCGAGGCGGGGGCGGCGGC.....GGGCCATGTCCCCGATGTCA 348

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 348 | 100.0 | 657 | 10 | ADD25846 | Add25846 Binding d |
| 2 | 348 | 100.0 | 1582 | 2 | AAX08910 | Aax08910 Human FAD |
| 3 | 348 | 100.0 | 1642 | 2 | AAT39397 | Aat39397 FADD (Fas |
| 4 | 348 | 100.0 | 1642 | 10 | ADD25622 | Add25622 Binding d |
| 5 | 348 | 100.0 | 1642 | 10 | ADD25628 | Add25628 Binding d |
| 6 | 348 | 100.0 | 1642 | 10 | ADE85083 | Ade85083 Farnesyl |
| 7 | 348 | 100.0 | 1642 | 10 | ADF81575 | Adf81575 Leukaemia |
| 8 | 348 | 100.0 | 1642 | 11 | ADI32159 | Adi32159 Human cDN |
| 9 | 348 | 100.0 | 1642 | 13 | ACN39272 | Acn39272 Tumour-as |
| 10 | 348 | 100.0 | 1701 | 2 | AAT30372 | Aat30372 MORT-1 cD |
| 11 | 348 | 100.0 | 1701 | 2 | AAT61397 | Aat61397 MORT-1 co |
| 12 | 348 | 100.0 | 1701 | 3 | AAZ44745 | Aaz44745 Human FAD |
| 13 | 346.4 | 99.5 | 606 | 2 | AAV71928 | Aav71928 MORT1 iso |
| 14 | 344.8 | 99.1 | 606 | 2 | AAV71929 | Aav71929 MORT1 iso |
| 15 | 344.8 | 99.1 | 627 | 2 | AAV71930 | Aav71930 MORT1 iso |
| 16 | 334.4 | 96.1 | 2288 | 12 | ADQ22935 | Adq22935 Human sof |
| 17 | 240.8 | 69.2 | 1813 | 12 | ADF77121 | Adf77121 Human NAP |
| 18 | 169.2 | 48.6 | 645 | 10 | ADD25856 | Add25856 Binding d |
| 19 | 169.2 | 48.6 | 1377 | 4 | AAC85064 | Aac85064 Mouse apo |
| 20 | 151.6 | 43.6 | 285 | 6 | ABX13073 | Abx13073 Fas-assoc |
| 21 | 148.4 | 42.6 | 285 | 6 | ABX13071 | Abx13071 Fas-assoc |
| 22 | 145.2 | 41.7 | 285 | 6 | ABX13075 | Abx13075 Fas-assoc |
| 23 | 145.2 | 41.7 | 285 | 6 | ABX13077 | Abx13077 Fas-assoc |
| 24 | 96.2 | 27.6 | 474 | 9 | ACH41827 | Ach41827 Human foe |
| 25 | 43.6 | 12.5 | 10732 | 3 | AAA10594 | Aaa10594 Gene enco |
| c 26 | 41 | 11.8 | 485 | 4 | AAI12429 | Aai12429 Probe #23 |
| c 27 | 41 | 11.8 | 485 | 4 | ABA54136 | Aba54136 Human foe |
| c 28 | 41 | 11.8 | 485 | 4 | AAI33785 | Aai33785 Probe #24 |
| c 29 | 41 | 11.8 | 485 | 4 | ABA43679 | Aba43679 Human bre |
| c 30 | 41 | 11.8 | 485 | 4 | ABA23882 | Aba23882 Probe #23 |
| c 31 | 41 | 11.8 | 485 | 4 | AAK27850 | Aak27850 Human bon |
| c 32 | 41 | 11.8 | 485 | 4 | AAK02405 | Aak02405 Human bra |
| c 33 | 41 | 11.8 | 485 | 4 | ABS27430 | Abs27430 Human liv |
| c 34 | 41 | 11.8 | 485 | 5 | AAI02343 | Aai02343 Probe #23 |
| c 35 | 41 | 11.8 | 485 | 6 | ABS02306 | Abs02306 Human gen |
| 36 | 39.8 | 11.4 | 4031 | 6 | ABQ91993 | Abq91993 Human NF- |
| 37 | 38.6 | 11.1 | 6023 | 11 | ADL22578 | Adl22578 Human dis |
| 38 | 38.2 | 11.0 | 801 | 11 | ABD06544 | Abd06544 Pseudomon |
| c 39 | 38.2 | 11.0 | 1269 | 11 | ABD06433 | Abd06433 Pseudomon |
| 40 | 38.2 | 11.0 | 2031 | 11 | ABD06576 | Abd06576 Pseudomon |
| 41 | 37.2 | 10.7 | 484 | 13 | ADR62984 | Adr62984 Cotton cD |
| 42 | 37.2 | 10.7 | 3051 | 10 | ADB62829 | Adb62829 Human cDN |
| 43 | 36.6 | 10.5 | 478 | 9 | ACH15546 | Ach15546 Human adu |
| 44 | 36.6 | 10.5 | 1339 | 4 | ABA09497 | Aba09497 Human ace |
| 45 | 36.6 | 10.5 | 1428 | 6 | ABK71541 | Abk71541 Human dit |

ALIGNMENTS

RESULT 1
ADD25846
ID ADD25846 standard; DNA; 657 BP.
XX
AC ADD25846;
XX
DT 15-JAN-2004 (first entry)
XX
DE Binding domain-immunoglobulin fusion protein-associated DNA #225.
XX
KW ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS Unidentified.
XX
PN US2003118592-A1.
XX
PD 26-JUN-2003.
XX
PF 25-JUL-2002; 2002US-00207655.
XX
PR 17-JAN-2001; 2001US-0367358P.
PR 17-JAN-2002; 2002US-00053530.
PR 03-JUN-2002; 2002US-0385691P.
XX
PA (GENE-) GENECRAFT INC.
XX
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX
DR WPI; 2003-801317/75.
XX
PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 407; 157pp; English.
XX

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CC   Unidentified
XX
SQ   Sequence 657 BP; 142 A; 193 C; 211 G; 111 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 348;  DB 10;  Length 657;
  Best Local Similarity   100.0%;  Pred. No. 3e-93;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 312

Qy         61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 372

Qy        121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 432

Qy        181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 492

Qy        241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 552

Qy        301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 600


RESULT 2
AAX08910
ID   AAX08910 standard; cDNA; 1582 BP.
XX
AC   AAX08910;
XX
DT   27-APR-1999  (first entry)
XX
DE   Human FADD protein coding sequence.
XX
KW   FIP; FADD interacting protein; FADD;
KW   Fas-associated protein with a novel death domain; cell death; apoptosis;
KW   Alzheimer's disease; Acquired Immune Deficiency Syndrome; AIDS;
KW   muscular dystrophy; amyotrophic lateral sclerosis; virus; bacteria;
KW   fungus; mycoplasm; protozoa; neoplasia; dysplasia; hyperplasia; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             70. .696
FT                   /*tag=  a
FT                   /label= Human_FADD_protein
XX
PN   WO9900499-A1.
XX
PD   07-JAN-1999.
XX
PF   26-JUN-1998;   98WO-US013320.
XX
PR   26-JUN-1997;   97US-0050792P.
PR   03-JUN-1998;   98US-0087886P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Chen TT,  Williams LT;
XX
DR   WPI; 1999-095745/08.
DR   P-PSDB; AAW96154.
XX
PT   New FADD (Fas-associated protein with a novel death domain)-Interacting
PT   Protein - useful for inducing or preventing apoptosis in a cell, to aid
PT   in controlling apoptosis-related diseases.
XX
PS   Disclosure; Page 45-46; 58pp; English.
XX
CC   An epitope of human FADD (Fas-associated protein with a novel death
CC   domain)-Interacting protein (FIP protein) comprising amino acids 348-727
CC   of the protein described in AAW96153, can be used to induce or prevent
CC   apoptosis in a cell. Specifically, decreasing the levels of FIP348-727
CC   prevents apoptosis. This is useful in cells which are dying prematurely,
CC   eg: Alzheimer's disease, Acquired Immune Deficiency Syndrome (AIDS),
CC   muscular dystrophy, amyotrophic lateral sclerosis (and other muscle
CC   wasting diseases), autoimmune diseases, and diseases where cells are
CC   infected with a pathogen (virus, bacteria, fungus, mycoplasm or
CC   protozoa). Increasing the levels of FIP 348-727 induces apoptosis which
CC   is useful in cells suffering from neoplasias, dysplasias, hyperplasias,
CC   or their symptoms. Purified and isolated FIP subgenomic polynucleotides
CC   are useful as primers to obtain more copies of the nucleotides, and as
CC   probes that identify wild-type or mutant coding sequences. They are also
CC   useful for expressing FIP mRNA, proteins or fusion proteins, and in the
CC   generation of FIP antisense oligonucleotides and ribozymes. They are also
CC   useful in expression constructs and in gene delivery vehicles (optionally
CC   in combination with a condensing agent) that deliver FIP mRNA or
CC   oligonucleotides, FIP proteins (including variants), FIP-specific
CC   ribozymes or single-chain antibodies into eukaryotic cells. This is the
CC   human FADD protein gene. Human FIP protein binds to amino acids 1-110 of
CC   the human FADD protein given in AAW96154
XX
SQ   Sequence 1582 BP; 344 A; 433 C; 483 G; 322 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 348;  DB 2;  Length 1582;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-93;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 372

Qy         61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 432

Qy        121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 492

Qy        181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
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Db        493 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 552

Qy        241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 612

Qy        301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 660


RESULT 3
AAT39397
ID   AAT39397 standard; cDNA; 1642 BP.
XX
AC   AAT39397;
XX
DT   22-FEB-1997  (first entry)
XX
DE   FADD (Fas-associating protein with novel death domain) gene.
XX
KW   Human; FADD; Fas-associating protein with novel death domain; apoptosis;
KW   Fas receptor; death domain; gene therapy; antibody; immunoassay;
KW   drug screening; diagnostic; AIDS; antiinflammatory; antitumour;
KW   cerebroprotective; neuroprotective; ss.
```

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XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  a
FT   misc_feature    4. .6
FT                   /*tag=  b
FT                   /note= "In-frame stop codon"
FT   CDS             130. .756
FT                   /*tag=  c
FT                   /product= "FADD protein"
FT   misc_feature    133. .501
FT                   /*tag=  d
FT                   /note= "Encodes N-terminal half, inducing apoptosis but
FT                   not binding Fas receptor"
FT   misc_feature    198
FT                   /*tag=  e
FT                   /note= "Clone 15 start point"
FT   misc_feature    249
FT                   /*tag=  f
FT                   /note= "Clone 8 start point"
FT   misc_feature    460. .660
FT                   /*tag=  g
FT                   /note= "Region encoding death domain"
FT   3'UTR           757. .1642
FT                   /*tag=  h
FT   polyA_signal    1636. .1641
FT                   /*tag=  i
XX
PN   WO9631603-A2.
XX
PD   10-OCT-1996.
XX
PF   28-FEB-1996;   96WO-US002857.
XX
PR   03-APR-1995;   95US-00416379.
PR   18-MAY-1995;   95US-00443982.
XX
PA   (UNMI ) UNIV MICHIGAN.
XX
PI   Dixit VM,  Orourke K;
XX
DR   WPI; 1996-465026/46.
DR   P-PSDB; AAW03653.
XX
PT   FADD protein that binds to cytoplasmic region of Fas receptor - for
PT   identifying inhibitors of Fas-associated apoptosis useful for treating
PT   e.g. AIDS, leukaemia, stroke, etc.
XX
PS   Example 1; Fig 2A-B; 96pp; English.
XX
CC   The sequence encodes FADD (Fas-associating protein with novel death
CC   domain), which binds the cytoplasmic region of a Fas receptor, and
CC   modulates apoptosis induced by activation of the receptor by ligand
CC   binding. The cDNA has been isolated using a yeast two-hybrid system which
CC   screens for proteins interacting with the Fas cytoplasmic domain. A GAL4
CC   DNA-binding domain has been fused to the human Fas antigen cytoplasmic
CC   tail to form a bait plasmid, which is used with a prey plasmid,
CC   containing a human B-lymphocyte cDNA library fused to the GAL4-activation
CC   domain, to co-transform yeast cells. Overlapping clones 8 and 15 have
CC   been isolated, and the full-length cDNA has been isolated from a human
CC   umbilical vein endothelial cell (HUVEC) library using clone 15 as a
CC   probe. The cDNA has an in-frame stop codon 130 bp upstream of the
CC   initiator Met. The encoded protein contains a death domain, with
CC   interacts with the death domain of Fas. The DNA may be used in gene
CC   therapy, and the protein or a corresponding antibody may be used to
CC   screen for agents modulating FADD pathway cellular functions and Fas-
CC   associated apoptosis, for use in therapy of e.g. AIDS, inflammation,
CC   leukaemia, myocardial infarction, degenerative disease, etc
XX
SQ   Sequence 1642 BP; 354 A; 448 C; 508 G; 332 T; 0 U; 0 Other;
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```
 Query Match           100.0%;  Score 348;  DB 2;  Length 1642;
 Best Local Similarity  100.0%;  Pred. No. 4.2e-93;
 Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 432

Qy         61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 492

Qy        121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 552

Qy        181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 612

Qy        241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 672

Qy        301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 720
```

```
RESULT 4
ADD25622
ID   ADD25622 standard; DNA; 1642 BP.
XX
AC   ADD25622;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated DNA #95.
XX
KW   ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 183; 157pp; English.
XX
CC   Unidentified
```

```
XX
SQ   Sequence 1642 BP; 354 A; 448 C; 508 G; 332 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 348;  DB 10;  Length 1642;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-93;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 432

Qy         61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 492

Qy        121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 552

Qy        181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 612

Qy        241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 672

Qy        301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 720


RESULT 5
ADD25628
ID   ADD25628 standard; DNA; 1642 BP.
XX
AC   ADD25628;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated DNA #98.
XX
KW   ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 189; 157pp; English.
XX
CC   Unidentified
XX
SQ   Sequence 1642 BP; 354 A; 448 C; 508 G; 332 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 348;  DB 10;  Length 1642;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-93;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 432

Qy         61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 492

Qy        121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 552

Qy        181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 612

Qy        241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 672

Qy        301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 720


RESULT 6
ADE85083
ID   ADE85083 standard; DNA; 1642 BP.
XX
AC   ADE85083;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Farnesyl transferase inhibitor modulated leukemia associated gene #302.
XX
KW   ss; cytostatic; farnesyl transferase inhibitor; gene expression;
KW   quinolinone; leukemia; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2003038129-A2.
XX
PD   08-MAY-2003.
XX
PF   30-OCT-2002; 2002WO-US034784.
XX
PR   30-OCT-2001; 2001US-0338997P.
PR   30-OCT-2001; 2001US-0340081P.
PR   30-OCT-2001; 2001US-0340938P.
PR   30-OCT-2001; 2001US-0341012P.
XX
PA   (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI   Raponi M;
XX
DR   WPI; 2003-513497/48.
XX
PT   Determining whether a patient will respond to treatment with a farnesyl
PT   transferase inhibitor, by analyzing the expression of gene that is
PT   differentially modulated in the presence of the inhibitor.
XX
PS   Disclosure; SEQ ID NO 302; 346pp; English.
XX
```

```
CC   The invention relates to a method of determining whether a patient will
CC   respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC   analyzing the expression of gene that is differentially modulated in the
CC   presence of an FTI. The method is useful for determining whether a
CC   patient will respond to treatment with a FTI such as (B)-6-[amino(4-
CC   chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
CC   methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a
CC   patient with leukemia with FTI if the analysis indicates that the patient
CC   will respond. This sequence corresponds to a gene whose expression may be
CC   modulated in the presence of FTI.
XX
SQ   Sequence 1642 BP; 354 A; 448 C; 508 G; 332 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 348;  DB 10;  Length 1642;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-93;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 432

Qy         61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 492

Qy        121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 552

Qy        181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 612

Qy        241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 672

Qy        301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 720


RESULT 7
ADF81575
ID   ADF81575 standard; DNA; 1642 BP.
XX
AC   ADF81575;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Leukaemia-related DNA sequence #2131.
XX
KW   Cytostatic; Gene therapy; leukaemia; ss.
XX
OS   Unidentified.
XX
PN   WO2003039443-A2.
XX
PD   15-MAY-2003.
XX
PF   04-NOV-2002; 2002WO-EP012303.
XX
PR   05-NOV-2001; 2001EP-00126244.
PR   30-APR-2002; 2002EP-00009758.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA   (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA   (HAFE/) HAFERLACH T.
PA   (SCHO/) SCHOCH C.
PA   (KERN/) KERN W.
XX
PI   Haferlach T,  Schoch C,  Kern W,  Kohlmann A,  Schnittger S,  Dugas M;
PI   Eils R,  Brors B,  Mergenthaler S;
XX
DR   WPI; 2003-505037/47.
XX
PT   Determining the subtype of leukemia cells and whether a patient sample
PT   contains leukemia cells or other cells, useful for treating leukemia,
PT   comprises determining the expression profile of a group of markers in a
PT   patient sample.
XX
PS   Disclosure; SEQ ID NO 2131; 2938pp; English.
XX
CC   The present invention relates to a method (M1) for determining the
CC   subtype of leukaemia cells and whether a patient sample contains
CC   leukaemia cells. The method comprises determining the expression profile
CC   of a group of markers in a patient sample. The method is useful for
CC   determining the presence of leukaemia cells, its types or subtypes, and
CC   for the preparation of a medicament for treating leukaemia.
XX
SQ   Sequence 1642 BP; 354 A; 448 C; 508 G; 332 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 348;  DB 10;  Length 1642;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-93;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 432

Qy         61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 492

Qy        121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 552

Qy        181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 612

Qy        241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 672

Qy        301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 720


RESULT 8
ADI32159
ID   ADI32159 standard; cDNA; 1642 BP.
XX
AC   ADI32159;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Human cDNA #1485.
XX
KW   Human; gene; ss; immunological response; immunopathological condition;
KW   Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW   irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW   acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW   osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS   Homo sapiens.
XX
PN   US6607879-B1.
XX
PD   19-AUG-2003.
XX
PF   09-FEB-1998;   98US-00023655.
XX
PR   09-FEB-1998;   98US-00023655.
```

XX
PA (INCY-) INCYTE CORP.
XX
PI Cocks BG, Stuart SG, Seilhamer JJ;
XX
DR WPI; 2003-895307/82.
XX
PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.
XX
PS Claim 1; SEQ ID NO 1485; 50pp; English.
XX
CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1642 BP; 354 A; 448 C; 508 G; 332 T; 0 U; 0 Other;

Query Match 100.0%; Score 348; DB 11; Length 1642;
Best Local Similarity 100.0%; Pred. No. 4.2e-93;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
Db 373 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 432

Qy 61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
Db 433 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 492

Qy 121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
Db 493 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 552

Qy 181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
Db 553 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 612

Qy 241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
Db 613 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 672

Qy 301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
Db 673 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 720

RESULT 9
ACN39272
ID ACN39272 standard; cDNA; 1642 BP.
XX
AC ACN39272;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) cDNA DNA103474, SEQ ID NO:3313.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
DR P-PSDB; ABM81285.
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 1; SEQ ID NO 3313; 7273pp; English.
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT nucleic acid of the invention
XX
SQ Sequence 1642 BP; 354 A; 448 C; 508 G; 332 T; 0 U; 0 Other;

Query Match 100.0%; Score 348; DB 13; Length 1642;
Best Local Similarity 100.0%; Pred. No. 4.2e-93;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
Db 373 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 432

```
Qy          61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         433 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 492

Qy         121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         493 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 552

Qy         181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         553 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 612

Qy         241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         613 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 672

Qy         301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db         673 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 720
```

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RESULT 10
AAT30372
ID   AAT30372 standard; cDNA; 1701 BP.
XX
AC   AAT30372;
XX
DT   13-SEP-1996  (first entry)
XX
DE   MORT-1 cDNA.
XX
KW   MORT-1; HF1; FAS/APO1 receptor; FAS-R; tumour; cancer; HIV;
KW   mediator of receptor toxicity; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .771
FT                   /*tag=  a
XX
PN   WO9618641-A1.
XX
PD   20-JUN-1996.
XX
PF   14-DEC-1995;   95WO-US016542.
XX
PR   15-DEC-1994;   94IL-00112022.
PR   19-FEB-1995;   95IL-00112692.
PR   16-JUL-1995;   95IL-00114615.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
PA   (WEIN/) WEINWURZEL H.
XX
PI   Wallach D,  Boldin M,  Varfolomeev E,  Mett I;
XX
DR   WPI; 1996-300569/30.
DR   P-PSDB; AAR98346.
XX
PT   MORT-1 protein capable of interacting with FAS-R intracellular domain -
PT   useful for modulating FAS-R ligand effect on cells and treating, e.g.
PT   tumour cells and HIV-infected cells.
XX
PS   Claim 3; Fig 4; 72pp; English.
XX
CC   A cDNA clone (AAT30372) codes for MORT-1 (AAR98346) (Mediator of Receptor
CC   Toxicity), also designated HF1, a novel protein that binds to the
CC   intracellular domain (Fas-IC) of the FAS ligand receptor FAS-R (or
CC   FAS/APO1), and is capable of modulating the function of Fas-R. It was
CC   obtd. from HeLa cells using a yeast 2-hybrid screen and 2-hybrid beta-
CC   galactosidase expression system. The cDNA can be used for prodn. of
CC   recombinant MORT-1 using transformed host cells. It can also be used to
CC   modulate the FAS-R ligand on cells carrying an FAS-R and to develop
CC   methods for the gene therapy of e.g. cancer and HIV infection
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XX
SQ   Sequence 1701 BP; 382 A; 459 C; 517 G; 343 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 348;  DB 2;  Length 1701;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-93;
  Matches  348;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         388 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 447

Qy          61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         448 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 507

Qy         121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         508 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 567

Qy         181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         568 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 627

Qy         241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         628 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 687

Qy         301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db         688 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 735
```

```
RESULT 11
AAT61397
ID   AAT61397 standard; cDNA; 1701 BP.
XX
AC   AAT61397;
XX
DT   25-MAR-2003  (revised)
DT   29-OCT-1997  (first entry)
XX
DE   MORT-1 coding sequence.
XX
KW   MACH; MORT-1 binding protein; mediator of receptor toxicity; cell death;
KW   antibody; FAS ligand receptor; FAS-R; death domain region; septic shock;
KW   tumour necrosis factor; tumour; HIV-infection; oligodendrocyte death;
KW   apoptosis/programmed cell death; p55-R; graft rejection; acute hepatitis;
KW   autoimmune disease; multiple sclerosis; AIDS-inhibited T-cell suicide;
KW   TNF; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .771
FT                   /*tag=  a
FT                   /product= "mediator of cellular toxicity (MORT-1)
FT                   protein"
XX
PN   WO9703998-A1.
XX
PD   06-FEB-1997.
XX
PF   14-JUN-1996;   96WO-US010521.
XX
PR   16-JUL-1995;   95IL-00114615.
PR   17-AUG-1995;   95IL-00114986.
PR   14-SEP-1995;   95IL-00115319.
PR   27-DEC-1995;   95IL-00116588.
PR   16-APR-1996;   96IL-00117932.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
PA   (WEIN/) WEINWURZEL H.
XX
```

PI Wallach D, Boldin M, Goncharov T, Goltsev YV;
XX
DR WPI; 1997-132570/12.
DR P-PSDB; AAW11894.
XX
PT New DNA encoding MACH protein that interacts with MORT-1 protein - to
PT mediate intracellular effects of FAS or TNF receptors, partic. for
PT regulating apoptosis in tumours, virus-infected cells etc.
XX
PS Disclosure; Page 102-103; 163pp; English.
XX
CC This sequence represents the coding sequence for the mediator of cellular
CC toxicity (MORT-1) protein. The protein encoded by this sequence is bound
CC by the protein of the invention (see AAW11892), designated MACH. MORT-1
CC binds to the FAS ligand receptor (FAS-R) death domain region, and
CC triggers part of the cell death signalling cascade in mammalian cells.
CC Vectors containing MACH, the MACH protein, and antibodies (Ab) against it
CC are used to modulate the effect of FAS-R ligand or TNF on cells that
CC carry FAS-R or p55-R. This is specifically for treating tumours, HIV-
CC infected cells or other diseased cells, by control of
CC apoptosis/programmed cell death. The MACH protein is a mediator of the
CC cell death pathway initiated by TNF and FAS-R binding, i.e. it mimics or
CC enhances the effect of MORT-1 where increased cytotoxicity is required.
CC To inhibit the effect of MORT-1, e.g. in cases of septic shock, graft
CC rejection and acute hepatitis, sequences encoding antisense molecules or
CC ribozymes, or Ab against MACH, are used. Compounds that inhibit MACH are
CC potentially useful for controlling MACH activity e.g. in cases of
CC autoimmune disease, oligodendrocyte death in multiple sclerosis or AIDS-
CC inhibited T-cell suicide. The MACH protein can also be used to isolate
CC and characterise other proteins and receptors involved in signalling and
CC for Ab production. The Ab can be used to purify the new proteins and for
CC diagnosis of conditions involving abnormal function of FAS-R mediated
CC cellular effects. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 1701 BP; 382 A; 459 C; 517 G; 343 T; 0 U; 0 Other;

Query Match 100.0%; Score 348; DB 2; Length 1701;
Best Local Similarity 100.0%; Pred. No. 4.3e-93;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 447

Qy         61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 507

Qy        121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 567

Qy        181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 627

Qy        241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 687

Qy        301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 735
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RESULT 12
AAZ44745
ID AAZ44745 standard; DNA; 1701 BP.
XX
AC AAZ44745;
XX
DT 19-APR-2000 (first entry)
XX
DE Human FADD DNA.
XX
KW FADD; human; antisense; inhibitor; Fas-associated death domain; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 145. .771
FT /*tag= a
FT /product= "FADD"
XX
PN US6015712-A.
XX
PD 18-JAN-2000.
XX
PF 19-JUL-1999; 99US-00357072.
XX
PR 19-JUL-1999; 99US-00357072.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowsert LM, Baker BF, Zhang H;
XX
DR WPI; 2000-126316/11.
DR P-PSDB; AAY51329.
XX
PT Antisense oligonucleotides, useful for inhibiting human Fas-associated
PT death domain (FADD) expression are targeted to the 3' untranslated region
PT of the FADD gene.
XX
PS Example 13; Col 43-46; 37pp; English.
XX
CC This invention describes novel antisense oligonucleotides (OGNs) (I) 8-20
CC nucleotides in length that specifically hybridize with and inhibit
CC nucleic acids encoding human Fas-associated death domain (FADD), targeted
CC to the 3' untranslated region (3'UTR). (I) can be used to treat animals,
CC especially humans, suspected of having or being prone to a disease or
CC condition associated with FADD expression. This sequence encodes the
CC human FADD protein described in the method of the invention
XX
SQ Sequence 1701 BP; 382 A; 459 C; 517 G; 343 T; 0 U; 0 Other;

Query Match 100.0%; Score 348; DB 3; Length 1701;
Best Local Similarity 100.0%; Pred. No. 4.3e-93;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 447

Qy         61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 507

Qy        121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 567

Qy        181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 627

Qy        241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 687

Qy        301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 735
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RESULT 13
AAV71928

```
ID   AAV71928 standard; cDNA; 606 BP.
XX
AC   AAV71928;
XX
DT   12-FEB-1999  (first entry)
XX
DE   MORT1 isoform MORT1del21 from NTERA2 cells encoding cDNA.
XX
KW   MORT1; MORT1del21; NTERA2; CNS; isoform; death domain; Fas/APO1;
KW   MACH alpha1; ICE/Ced3; caspase; anti-apoptopic; gene therapy;
KW   in vivo agent; neuronal apoptosis; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .606
FT                   /*tag=  a
FT                   /product= "MORT1del21"
XX
PN   WO9849297-A1.
XX
PD   05-NOV-1998.
XX
PF   14-APR-1998;   98WO-US007439.
XX
PR   25-APR-1997;   97US-0044835P.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Bingham BW,  Young KH,  Wood AT,  Birsan C;
XX
DR   WPI; 1999-009424/01.
DR   P-PSDB; AAW87491.
XX
PT   Human, neuronal MORT1 iso:form(s) - used as screening agents in
PT   diagnosing CNS diseases, and in discovering CNS-specific anti-apoptopic
PT   compounds.
XX
PS   Claim 1; Page 26-27; 31pp; English.
XX
CC   This represents a cDNA sequence of a MORT1 isoform MORT1del21, isolated
CC   from NTERA2 cells and deposited under the accession number ATCC 209013.
CC   This sequence has a 21 base pair deletion as compared to the published
CC   MORT1 sequence (bp 172-192 of the coding sequence). The invention relates
CC   to three MORT1 nucleic acid isoforms (AAV71928 to AAV71930) that encode
CC   proteins which can interact with the death domain of Fas/APO1. The MORT1
CC   isoforms can also interact with MACH alpha1 or other members of the
CC   ICE/Ced3 (Caspase) family of proteins. The transcript isoforms, together
CC   with their encoded proteins are useful as screening agents in diagnosing
CC   CNS diseases, and in discovering CNS-specific anti-apoptopic compounds.
CC   They are useful in gene therapy either as in vivo agents in humans or as
CC   experimental tools in manipulating neuronal apoptosis in cell culture and
CC   animal model systems
XX
SQ   Sequence 606 BP; 128 A; 176 C; 200 G; 102 T; 0 U; 0 Other;

  Query Match             99.5%;  Score 346.4;  DB 2;  Length 606;
  Best Local Similarity   99.7%;  Pred. No. 8.7e-93;
  Matches  347;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
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Db        223 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 282

Qy         61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 342

Qy        121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 402

Qy        181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 462

Qy        241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        463 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGGGGTTCAG 522

Qy        301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 570


RESULT 14
AAV71929
ID   AAV71929 standard; cDNA; 606 BP.
XX
AC   AAV71929;
XX
DT   12-FEB-1999  (first entry)
XX
DE   MORT1 isoform MORT1del21 from brain cells encoding cDNA.
XX
KW   MORT1; MORT1del21; NTERA2; CNS; isoform; death domain; Fas/APO1;
KW   MACH alpha1; ICE/Ced3; caspase; anti-apoptopic; gene therapy;
KW   in vivo agent; neuronal apoptosis; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .606
FT                   /*tag=  a
FT                   /product= "MORT1del21"
XX
PN   WO9849297-A1.
XX
PD   05-NOV-1998.
XX
PF   14-APR-1998;   98WO-US007439.
XX
PR   25-APR-1997;   97US-0044835P.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Bingham BW,  Young KH,  Wood AT,  Birsan C;
XX
DR   WPI; 1999-009424/01.
DR   P-PSDB; AAW87492.
XX
PT   Human, neuronal MORT1 iso:form(s) - used as screening agents in
PT   diagnosing CNS diseases, and in discovering CNS-specific anti-apoptopic
PT   compounds.
XX
PS   Claim 2; Page 28-29; 31pp; English.
XX
CC   This represents a cDNA sequence of a MORT1 isoform MORT1del21, isolated
CC   from human brain and deposited under the accession number ATCC 209018.
CC   This sequence has a 21 base pair deletion as compared to the published
CC   MORT1 sequence (bp 172-192 of the coding sequence). The invention relates
CC   to three MORT1 nucleic acid isoforms (AAV71928 to AAV71930) that encode
CC   proteins which can interact with the death domain of Fas/APO1. The MORT1
CC   isoforms can also interact with MACH alpha1 or other members of the
CC   ICE/Ced3 (Caspase) family of proteins. The transcript isoforms, together
CC   with their encoded proteins are useful as screening agents in diagnosing
CC   CNS diseases, and in discovering CNS-specific anti-apoptopic compounds.
CC   They are useful in gene therapy either as in vivo agents in humans or as
CC   experimental tools in manipulating neuronal apoptosis in cell culture and
CC   animal model systems
XX
SQ   Sequence 606 BP; 130 A; 177 C; 198 G; 101 T; 0 U; 0 Other;

  Query Match             99.1%;  Score 344.8;  DB 2;  Length 606;
  Best Local Similarity   99.4%;  Pred. No. 2.6e-92;
  Matches  346;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
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Db        223 TTCGAGGCGGGGGCGGCAGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 282

Qy         61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 342

Qy        121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 402

Qy        181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 462

Qy        241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        463 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGCGGCTGACCTGGTACAAGAGGTTCAG 522

Qy        301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 570
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```
RESULT 15
AAV71930
ID   AAV71930 standard; cDNA; 627 BP.
XX
AC   AAV71930;
XX
DT   12-FEB-1999  (first entry)
XX
DE   MORT1 isoform MORT1G173A from human brain encoding cDNA.
XX
KW   MORT1; MORT1del21; NTERA2; CNS; isoform; death domain; Fas/APO1;
KW   MACH alpha1; ICE/Ced3; caspase; anti-apoptopic; gene therapy;
KW   in vivo agent; neuronal apoptosis; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .627
FT                   /*tag=  a
FT                   /product= "MORT1G173A"
XX
PN   WO9849297-A1.
XX
PD   05-NOV-1998.
XX
PF   14-APR-1998;   98WO-US007439.
XX
PR   25-APR-1997;   97US-0044835P.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Bingham BW,  Young KH,  Wood AT,  Birsan C;
XX
DR   WPI; 1999-009424/01.
DR   P-PSDB; AAW87493.
XX
PT   Human, neuronal MORT1 iso:form(s) - used as screening agents in
PT   diagnosing CNS diseases, and in discovering CNS-specific anti-apoptopic
PT   compounds.
XX
PS   Claim 3; Page 30-31; 31pp; English.
XX
CC   This represents a cDNA sequence of a MORT1 isoform MORT1G173A, isolated
CC   from human brain and deposited under the accession number ATCC 209019.
CC   This sequence has a nucleotide substitution (G to A) at basepair position
CC   173 of the published MORT1 coding sequence. The invention relates to
CC   three MORT1 nucleic acid isoforms (AAV71928 to AAV71930) that encode
CC   proteins which can interact with the death domain of Fas/APO1. The MORT1
CC   isoforms can also interact with MACH alpha1 or other members of the
CC   ICE/Ced3 (Caspase) family of proteins. The transcript isoforms, together
CC   with their encoded proteins are useful as screening agents in diagnosing
CC   CNS diseases, and in discovering CNS-specific anti-apoptopic compounds.
CC   They are useful in gene therapy either as in vivo agents in humans or as
CC   experimental tools in manipulating neuronal apoptosis in cell culture and
CC   animal model systems
XX
SQ   Sequence 627 BP; 134 A; 186 C; 204 G; 103 T; 0 U; 0 Other;
```

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  Query Match             99.1%;  Score 344.8;  DB 2;  Length 627;
  Best Local Similarity   99.4%;  Pred. No. 2.6e-92;
  Matches  346;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TTCGAGGCGGGGGCGGCGGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 60
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        244 TTCGAGGCGGGGGCGGCAGCCGGGGCCGCGCCTGGGGAAGAAGACCTGTGTGCAGCATTT 303

Qy         61 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AACGTCATATGTGATAATGTGGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC 363

Qy        121 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 423

Qy        181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG 483

Qy        241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG 300
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        484 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGCGGCTGACCTGGTACAAGAGGTTCAG 543

Qy        301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 591
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